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cont'd

consisted of 49 amino acids and contained a number of highly conserved Ser/Thr and Tyr phosphorylation sites (Fig 8A, residues in *italic*). The search of known patterns with the Prosite program identified the motifs SSk/SYK as protein kinase C, SKQD (amino acids 296-299 of SEQ ID NO.: 13)/TSEE (amino acids 275-278 of SEQ ID NO.: 13) as CK2 and KQDGESY(amino acids 276-281 of SEQ ID NO.: 13) /KHDGVNY(amino acids 287-293 of SEQ ID NO.: 13) as Tyrosine kinase phosphorylation signatures.

IN THE CLAIMS:

Kindly enter the following amended claims:

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1. (Amended) An isoalted polypeptide belonging to a subfamily of the human Immunoglobulin Superfamily, which polypeptide shows at least 70% sequence homology with the amino acid sequence of the murine Confluency Regulated Adhesion Molecule 1 (CRAM-1, SEQ ID NO: 13) or CRAM-2 (SEQ ID NO.: 14).

2. (Amended) The polypeptide as claimed in claim 1 comprising an amino acid sequence that is 70% to essentially 100% homologous to the amino acid sequence of human CRAM-1 (SEQ ID NO.: 15).

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11. (Amended) A polypeptide having at least part of the amino acid sequence of the polypeptide as claimed in claims 1 or 2 for use in the treatment of inflammation reactions.

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12. (Amended) The polypeptide as claimed in claim 11, wherein the at least part of the amino acid sequence comprises at least one of the extracellular domains VC2, and the membrane proximal cytoplasmic sequence defined by amino acids 266-272 of SEQ ID NO.: 13 or amino acids 261-267 of SEQ ID NO.: 14.

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13. The polypeptide as claimed in claims 1, or 2 in soluble form for use in modulating vascular permeability.